



SEQUENCE LISTING

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(1) GENERAL INFORMATION:

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- (i) APPLICANT: Lester, Henry A.
Davidson, Norman
Kofuji, Paulo

10 (ii) TITLE OF INVENTION: INWARD RECTIFIER, G-PROTEIN ACTIVATED,
MAMMALIAN, POTASSIUM CHANNELS AND USES THEREOF

(iii) NUMBER OF SEQUENCES: 6

15

(iv) CORRESPONDENCE ADDRESS:

- (A) ADDRESSEE: Flehr Hohbach Test Albritton & Herbert LLP
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(C) CITY: San Francisco
(D) STATE: California
20 (E) COUNTRY: United States
(F) ZIP: 94111-4187

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(v) COMPUTER READABLE FORM:

- (A) MEDIUM TYPE: Floppy disk
25 (B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30

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(vi) CURRENT APPLICATION DATA:

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- (A) APPLICATION NUMBER: US 09/039,927
(B) FILING DATE: 16-MAR-1998
(C) CLASSIFICATION:

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(vii) PRIOR APPLICATION DATA:

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- (A) APPLICATION NUMBER: US 08/066,371
(B) FILING DATE: 21-MAR-1993

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(viii) PRIOR APPLICATION DATA:

- (A) APPLICATION NUMBER: US 08/614,801
(B) FILING DATE: 07-MAR-1996

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(ix) ATTORNEY/AGENT INFORMATION:

- (A) NAME: Trecartin, Richard F.
(B) REGISTRATION NUMBER: 31,801
(C) REFERENCE/DOCKET NUMBER: A-63098-1/RFT

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(x) TELECOMMUNICATION INFORMATION:

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- (A) TELEPHONE: (415) 781-1989
(B) TELEFAX: (415) 398-3249
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(2) INFORMATION FOR SEQ ID NO:1:

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(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2070 base pairs
(B) TYPE: nucleic acid

(C) STRANDEDNESS: unknown
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA (genomic)

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(ix) FEATURE:

(A) NAME/KEY: CDS
(B) LOCATION: 32..1534

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

GGCACGAGAA	TCTGGATCTC	CCCTCCGTAT	T	ATG	TCT	GCA	CTC	CGA	AGG	AAA	52						
				Met	Ser	Ala	Leu	Arg	Arg	Lys							
15				1						5							
TTT	GGG	GAC	GAT	TAC	CAG	GTA	GTG	ACC	ACT	TCG	TCC	AGC	GGT	TCG	GGC	100	
Phe	Gly	Asp	Asp	Tyr	Gln	Val	Val	Thr	Thr	Ser	Ser	Ser	Gly	Ser	Gly		
10		15									20						
20	TTG	CAG	CCC	CAG	GGG	CCA	GGA	CAG	GGC	CCA	CAG	CAG	CTT	GTA	CCC	148	
Leu	Gln	Pro	Gln	Gly	Pro	Gly	Gln	Gly	Pro	Gln	Gln	Gln	Gln	Leu	Val	Pro	
25		30		35													
25	AAG	AAG	AAA	CGG	CAG	CGG	TTC	GTG	GAC	AAG	AAC	GGT	CGG	TGC	AAT	GTG	196
Lys	Lys	Arg	Gln	Arg	Phe	Val	Asp	Lys	Asn	Gly	Arg	Cys	Asn	Val			
40		45		50										55			
30	CAG	CAC	GGC	AAC	CTG	GGC	AGC	GAG	ACC	AGT	CGC	TAC	CTT	TCC	GAC	CTC	244
Gln	His	Gly	Asn	Leu	Gly	Ser	Glu	Thr	Ser	Arg	Tyr	Leu	Ser	Asp	Leu		
60		65		70													
35	TTC	ACT	ACC	CTG	GTG	GAT	CTC	AAG	TGG	CGT	TGG	AAC	CTC	TTT	ATC	TTC	292
Phe	Thr	Thr	Leu	Val	Asp	Leu	Lys	Trp	Arg	Trp	Asn	Leu	Phe	Ile	Phe		
75		80		85													
40	ATC	CTC	ACC	TAC	ACC	GTG	GCC	TGG	CTC	TTC	ATG	GCG	TCC	ATG	TGG	TGG	340
Ile	Leu	Thr	Tyr	Thr	Val	Ala	Trp	Leu	Phe	Met	Ala	Ser	Met	Trp	Trp		
90		95		100													
45	GTG	ATC	GCT	TAT	ACC	CGG	GGC	GAC	CTG	AAC	AAA	GCC	CAT	GTC	GGC	AAC	388
Val	Ile	Ala	Tyr	Thr	Arg	Gly	Asp	Leu	Asn	Lys	Ala	His	Val	Gly	Asn		
105		110		115													
50	TAC	ACT	CCC	TGT	GTG	GCC	AAT	GTC	TAT	AAC	TTC	CCC	TCT	GCC	TTC	CTT	436
Tyr	Thr	Pro	Cys	Val	Ala	Asn	Val	Tyr	Asn	Phe	Pro	Ser	Ala	Phe	Leu		
120		125		130									135				
55	TTC	TTC	ATC	GAG	ACC	GAG	GCC	ACC	ATC	GGC	TAT	GGC	TAC	CGC	TAC	ATC	484
Phe	Phe	Ile	Glu	Thr	Glu	Ala	Thr	Ile	Gly	Tyr	Gly	Tyr	Arg	Tyr	Ile		
140		145		150													
55	ACC	GAC	AAG	TGC	CCC	GAG	GGC	ATC	ATC	CTT	TTC	CTT	TTC	CAG	TCC	ATC	532
Thr	Asp	Lys	Cys	Pro	Glu	Gly	Ile	Ile	Leu	Phe	Leu	Phe	Gln	Ser	Ile		
155		160		165													

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	CTT GGC TCC ATC GTG GAC GCT TTC CTC ATC GGC TGC ATG TTC ATC AAG Leu Gly Ser Ile Val Asp Ala Phe Leu Ile Gly Cys Met Phe Ile Lys 170 175 180	580
5	ATG TCC CAG CCC AAA AAG CGC GCC GAG ACC CTC ATG TTT AGC GAG CAT Met Ser Gln Pro Lys Lys Arg Ala Glu Thr Leu Met Phe Ser Glu His 185 190 195	628
10	GCG GTT ATT TCC ATG AGG GAC GGA AAA CTC ACT CTC ATG TTC CGG GTG Ala Val Ile Ser Met Arg Asp Gly Lys Leu Thr Leu Met Phe Arg Val 200 205 210 215	676
15	GCG AAC CTG CGC AAC AGC CAC ATG GTC TCC GCG CAG ATC CGC TGC AAG Gly Asn Leu Arg Asn Ser His Met Val Ser Ala Gln Ile Arg Cys Lys 220 225 230	724
	CTG CTC AAA TCT CGG CAG ACA CCT GAG GGT GAG TTT CTA CCC CTT GAC Leu Leu Lys Ser Arg Gln Thr Pro Glu Gly Glu Phe Leu Pro Leu Asp 235 240 245	772
20	CAA CTT GAA CTG GAT GTA GGT TTT AGT ACA GGG GCA GAT CAA CTT TTT Gln Leu Glu Leu Asp Val Gly Phe Ser Thr Gly Ala Asp Gln Leu Phe 250 255 260	820
25	CTT GTG TCC CCT CTC ACC ATT TGC CAC GTG ATC GAT GCC AAA AGC CCC Leu Val Ser Pro Leu Thr Ile Cys His Val Ile Asp Ala Lys Ser Pro 265 270 275	868
30	TTT TAT GAC CTA TCC CAG CGA AGC ATG CAA ACT GAA CAG TTC GAG GTG Phe Tyr Asp Leu Ser Gln Arg Ser Met Gln Thr Glu Gln Phe Glu Val 280 285 290 295	916
35	GTC GTC ATC CTG GAA GGC ATC GTG GAA ACC ACA GGG ATG ACT TGT CAA Val Val Ile Leu Glu Gly Ile Val Glu Thr Thr Gly Met Thr Cys Gln 300 305 310	964
	GCT CGA ACA TCA TAC ACC GAA GAT GAA GTT CTT TGG GGT CAT CGT TTT Ala Arg Thr Ser Tyr Thr Glu Asp Glu Val Leu Trp Gly His Arg Phe 315 320 325	1012
40	TTC CCT GTA ATT TCT TTA GAA GAA GGA TTC TTT AAA GTC GAT TAC TCC Phe Pro Val Ile Ser Leu Glu Gly Phe Phe Lys Val Asp Tyr Ser 330 335 340	1060
45	CAG TTC CAT GCA ACC TTT GAA GTC CCC ACC CCT CCG TAC AGT GTG AAA Gln Phe His Ala Thr Phe Glu Val Pro Thr Pro Pro Tyr Ser Val Lys 345 350 355	1108
50	GAG CAG GAA GAA ATG CTT CTC ATG TCT TCC CCT TTA ATA GCA CCA GCC Glu Gln Glu Glu Met Leu Leu Met Ser Ser Pro Leu Ile Ala Pro Ala 360 365 370 375	1156
55	ATA ACC AAC AGC AAA GAA AGA CAC AAT TCT GTG GAG TGC TTA GAT GGA Ile Thr Asn Ser Lys Glu Arg His Asn Ser Val Glu Cys Leu Asp Gly 380 385 390	1204

	CTA GAT GAC ATT AGC ACA AAA CTT CCA TCG AAG CTG CAG AAA ATT ACG Leu Asp Asp Ile Ser Thr Lys Leu Pro Ser Lys Leu Gln Lys Ile Thr 395 400 405	1252
5	GGG AGA GAA GAC TTT CCC AAA AAA CTC CTG AGG ATG AGT TCT ACA ACT Gly Arg Glu Asp Phe Pro Lys Lys Leu Leu Arg Met Ser Ser Thr Thr 410 415 420	1300
10	TCA GAA AAA GCC TAT AGT TTG GGT GAT TTG CCC ATG AAA CTC CAA CGA Ser Glu Lys Ala Tyr Ser Leu Gly Asp Leu Pro Met Lys Leu Gln Arg 425 430 435	1348
15	ATA AGT TCG GTT CCT GGC AAC TCT GAA GAA AAA CTG GTA TCT AAA ACC Ile Ser Ser Val Pro Gly Asn Ser Glu Glu Lys Leu Val Ser Lys Thr 440 445 450 455	1396
20	ACC AAG ATG TTA TCA GAT CCC ATG AGC CAG TCT GTG GCC GAT TTG CCA Thr Lys Met Leu Ser Asp Pro Met Ser Gln Ser Val Ala Asp Leu Pro 460 465 470	1444
25	CCG AAG CTT CAA AAG ATG GCT GGA GGA CCT ACC AGG ATG GAA GGG AAT Pro Lys Leu Gln Lys Met Ala Gly Pro Thr Arg Met Glu Gly Asn 475 480 485	1492
30	CTT CCA GCC AAA CTA AGA AAA ATG AAC TCT GAC CGC TTC ACA Leu Pro Ala Lys Leu Arg Lys Met Asn Ser Asp Arg Phe Thr 490 495 500	1534
35	TAGCAAAACA CCCCCATTAGG CATTATTTCA TGTTTGATT TAGTTTAGT CCAATATTTG GCTGATAAGA TAATCCTCCC CGGGAAATCT GAGAGGTCTA TCCCAGTCTG GCAAATTCTAT CAGAGGACTC TTCATTGAAG TGTTGTTACT GTGTTGAACA TGAGTTACAA AGGGAGGACA TCATAAGAAA GCTAATAGTT GGCATGTATT ATCACATCAA GCATGCAATA ATGTGCAAAT TTTGCATTTA GTTTCTGGC ATGATTATA TATGGCATAT TTATATTGAA TATTCTGGAA AAATATATAA ATATATATTGAAAGTGGAGA TATTCTCCCC ATAATTTCTA ATATATGTAT TAAGCCAAAC ATGAGTGGAT AGCTTTCAGG GCACTAAAAT AATATACATG CATACTAC TACATGCATA TGCACAGACA CATAACACACA CATACTCATA TATATAAAAC ATACCCATAC AAACATATAT ATCTAATAAA AATTGTGATG TTTTGTCAA AAAAAAAA AAAAAA	1594 1654 1714 1774 1834 1894 1954 2014 2070
40		
45		

(2) INFORMATION FOR SEQ ID NO:2:

- 50 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 501 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
- 55 (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Ser Ala Leu Arg Arg Lys Phe Gly Asp Asp Tyr Gln Val Val Thr
 1 5 10 15

5 Thr Ser Ser Ser Gly Ser Gly Leu Gln Pro Gln Gly Pro Gly Gln Gly
 20 25 30

10 Pro Gln Gln Gln Leu Val Pro Lys Lys Lys Arg Gln Arg Phe Val Asp
 35 40 45

Lys Asn Gly Arg Cys Asn Val Gln His Gly Asn Leu Gly Ser Glu Thr
 50 55 60

15 Ser Arg Tyr Leu Ser Asp Leu Phe Thr Thr Leu Val Asp Leu Lys Trp
 65 70 75 80

Arg Trp Asn Leu Phe Ile Phe Ile Leu Thr Tyr Thr Val Ala Trp Leu
 85 90 95

20 Phe Met Ala Ser Met Trp Trp Val Ile Ala Tyr Thr Arg Gly Asp Leu
 100 105 110

25 Asn Lys Ala His Val Gly Asn Tyr Thr Pro Cys Val Ala Asn Val Tyr
 115 120 125

Asn Phe Pro Ser Ala Phe Leu Phe Phe Ile Glu Thr Glu Ala Thr Ile
 130 135 140

30 Gly Tyr Gly Tyr Arg Tyr Ile Thr Asp Lys Cys Pro Glu Gly Ile Ile
 145 150 155 160

Leu Phe Leu Phe Gln Ser Ile Leu Gly Ser Ile Val Asp Ala Phe Leu
 165 170 175

35 Ile Gly Cys Met Phe Ile Lys Met Ser Gln Pro Lys Lys Arg Ala Glu
 180 185 190

Thr Leu Met Phe Ser Glu His Ala Val Ile Ser Met Arg Asp Gly Lys
 40 195 200 205

Leu Thr Leu Met Phe Arg Val Gly Asn Leu Arg Asn Ser His Met Val
 210 215 220

45 Ser Ala Gln Ile Arg Cys Lys Leu Leu Lys Ser Arg Gln Thr Pro Glu
 225 230 235 240

Gly Glu Phe Leu Pro Leu Asp Gln Leu Glu Leu Asp Val Gly Phe Ser
 245 250 255

50 Thr Gly Ala Asp Gln Leu Phe Leu Val Ser Pro Leu Thr Ile Cys His
 260 265 270

Val Ile Asp Ala Lys Ser Pro Phe Tyr Asp Leu Ser Gln Arg Ser Met
 55 275 280 285

Gln Thr Glu Gln Phe Glu Val Val Val Ile Leu Glu Gly Ile Val Glu
 290 295 300

Thr Thr Gly Met Thr Cys Gln Ala Arg Thr Ser Tyr Thr Glu Asp Glu
 5 305 310 315 320

Val Leu Trp Gly His Arg Phe Phe Pro Val Ile Ser Leu Glu Glu Gly
 325 330 335

10 Phe Phe Lys Val Asp Tyr Ser Gln Phe His Ala Thr Phe Glu Val Pro
 340 345 350

Thr Pro Pro Tyr Ser Val Lys Glu Gln Glu Glu Met Leu Leu Met Ser
 355 360 365

15 Ser Pro Leu Ile Ala Pro Ala Ile Thr Asn Ser Lys Glu Arg His Asn
 370 375 380

Ser Val Glu Cys Leu Asp Gly Leu Asp Asp Ile Ser Thr Lys Leu Pro
 20 385 390 395 400

Ser Lys Leu Gln Lys Ile Thr Gly Arg Glu Asp Phe Pro Lys Lys Leu
 405 410 415

25 Leu Arg Met Ser Ser Thr Thr Ser Glu Lys Ala Tyr Ser Leu Gly Asp
 420 425 430

Leu Pro Met Lys Leu Gln Arg Ile Ser Ser Val Pro Gly Asn Ser Glu
 435 440 445

30 Glu Lys Leu Val Ser Lys Thr Thr Lys Met Leu Ser Asp Pro Met Ser
 450 455 460

Gln Ser Val Ala Asp Leu Pro Pro Lys Leu Gln Lys Met Ala Gly Gly
 35 465 470 475 480

Pro Thr Arg Met Glu Gly Asn Leu Pro Ala Lys Leu Arg Lys Met Asn
 485 490 495

40 Ser Asp Arg Phe Thr
 500

(2) INFORMATION FOR SEQ ID NO:3:

- 45 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1978 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: unknown
 (D) TOPOLOGY: unknown
- 50 (ii) MOLECULE TYPE: DNA (genomic)
- 55 (ix) FEATURE:
 (A) NAME/KEY: CDS
 (B) LOCATION: 488..1729

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

	GTCTCCCTGC AAGGTCTATC ACTTGCTCC TAAACGAGGA TTTATTCCCT CTGCCACTCA	60
5	AGGCTGTCCC CCAGTTCCCT CGCAACCGGG CTTCCCTCCTC AGTCCCTGCC CACACGCGCA	120
	CTCCTCTGCC CCGCGGTGGC CCCAGCGCCC AGCCCTCCAG CCAGAGGGAG CCAGGCACCA	180
10	GACGGCAGCA CCTGGCTGGA GAGGTTGGC GGGCCGAGGG TGGGGATCCG CGGGAACCGG	240
	CGAGTCGGAG CTGGAGCAGG AGCTGGACCC AACCGCTAGC AGCAGAATGG AGTCTCCTGA	300
	AAGCCTGCCG GGGCTGATGT GAAATTGGGC CATCTGCTTC CAGTTGGTCT GTTTCCCTCCT	360
15	TTTCTTGTAT TTTCTCCCT CGCCATTACAC CGTGGAGTGA ATTATTGAAT CTTGCTCCGT	420
	TCCGAGAGAG GCGATCAGGA TGGAGTGAAC CTACCCCTGTC CACTACAAGG AAAAGCACAA	480
20	AGAAGAA ATG ACA ATG GCC AAG TTA ACT GAA TCC ATG ACT AAC GTC TTG	529
	Met Thr Met Ala Lys Leu Thr Glu Ser Met Thr Asn Val Leu	
	1 5 10	
	GAA GGC GAT TCC ATG GAC CAG GAT GTG GAA AGC CCA GTG GCC ATT CAC	577
25	Glu Gly Asp Ser Met Asp Gln Asp Val Glu Ser Pro Val Ala Ile His	
	15 20 25 30	
	CAG CCA AAG TTG CCT AAG CAG GCC AGG GAC GAC CTG CCG AGA CAC ATC	625
	Gln Pro Lys Leu Pro Lys Gln Ala Arg Asp Asp Leu Pro Arg His Ile	
	35 40 45	
30	AGC CGA GAC AGG ACC AAA AGG AAA ATC CAG AGG TAC GTG AGG AAG GAT	673
	Ser Arg Asp Arg Thr Lys Arg Lys Ile Gln Arg Tyr Val Arg Lys Asp	
	50 55 60	
35	GGG AAG TGC AAC GTT CAC CAC GGC AAT GTG CGG GAG ACC TAC CGA TAC	721
	Gly Lys Cys Asn Val His His Gly Asn Val Arg Glu Thr Tyr Arg Tyr	
	65 70 75	
40	CTG ACG GAC ATC TTC ACC ACC CTG GTG GAC CTG AAG TGG AGA TTC AAC	769
	Leu Thr Asp Ile Phe Thr Thr Leu Val Asp Leu Lys Trp Arg Phe Asn	
	80 85 90	
45	CTG TTG ATC TTT GTC ATG GTC TAC ACA GTG ACG TGG CTT TTC TTT GGG	817
	Leu Leu Ile Phe Val Met Val Tyr Thr Val Thr Trp Leu Phe Phe Gly	
	95 100 105 110	
	ATG ATC TGG TGG CTG ATT GCG TAC ATC CGG GGA GAT ATG GAC CAC ATA	865
	Met Ile Trp Trp Leu Ile Ala Tyr Ile Arg Gly Asp Met Asp His Ile	
	115 120 125	
50	GAG GAC CCC TCG TGG ACT CCT TGT GTC ACC AAC CTC AAC GGG TTT GTC	913
	Glu Asp Pro Ser Trp Thr Pro Cys Val Thr Asn Leu Asn Gly Phe Val	
	130 135 140	

	TCT GCT TTT TTA TTC TCC ATA GAG ACA GAA ACC ACC ATC GGT TAT GGC Ser Ala Phe Leu Phe Ser Ile Glu Thr Glu Thr Thr Ile Gly Tyr Gly 145 150 155	961
5	TAC CGG GTC ATC ACG GAC AAG TGC CCT GAG GGG ATT ATT CTC CTC TTA Tyr Arg Val Ile Thr Asp Lys Cys Pro Glu Gly Ile Ile Leu Leu Leu 160 165 170	1009
10	ATC CAG TCC GTG TTG GGG TCC ATT GTC AAC GCC TTC ATG GTA GGA TGT Ile Gln Ser Val Leu Gly Ser Ile Val Asn Ala Phe Met Val Gly Cys 175 180 185 190	1057
15	ATG TTT GTG AAA ATA TCC CAA CCC AAG AAG AGG GCA GAG ACC CTG GTC Met Phe Val Lys Ile Ser Gln Pro Lys Lys Arg Ala Glu Thr Leu Val 195 200 205	1105
20	TTT TCC ACC CAC GCG GTG ATC TCC ATG CGG GAT GGG AAA CTG TGC TTG Phe Ser Thr His Ala Val Ile Ser Met Arg Asp Gly Lys Leu Cys Leu 210 215 220	1153
25	ATG TTC CGG GTG GGG GAC TTG AGG AAT TCT CAC ATT GTG GAG GCA TCC Met Phe Arg Val Gly Asp Leu Arg Asn Ser His Ile Val Glu Ala Ser 225 230 235	1201
30	ATC AGA GCC AAG TTG ATC AAG TCC AAA CAG ACT TCA GAG GGG GAG TTT Ile Arg Ala Lys Leu Ile Lys Ser Lys Gln Thr Ser Glu Gly Glu Phe 240 245 250	1249
35	ATT CCC CTC AAC CAG AGT GAT ATC AAC GTG GGG TAC TAC ACA GGG GAC Ile Pro Leu Asn Gln Ser Asp Ile Asn Val Gly Tyr Tyr Thr Gly Asp 255 260 265 270	1297
40	GAC CGG CTC TTT CTG GTG TCA CCA TTG ATT ATT AGC CAT GAA ATT AAC Asp Arg Leu Phe Leu Val Ser Pro Leu Ile Ile Ser His Glu Ile Asn 275 280 285	1345
45	CAA CAG AGT CCC TTC TGG GAG ATC TCC AAA GCG CAG CTG CCT AAA GAG Gln Gln Ser Pro Phe Trp Glu Ile Ser Lys Ala Gln Leu Pro Lys Glu 290 295 300	1393
50	GAA CTG GAG ATT GTG GTC ATC CTG GAG GGA ATC GTG GAA GCC ACA GGA Glu Leu Glu Ile Val Val Ile Leu Glu Gly Ile Val Glu Ala Thr Gly 305 310 315	1441
55	ATG ACG TGC CAA GCC CGA AGC TCC TAC ATC ACC AGT GAG ATC TTG TGG Met Thr Cys Gln Ala Arg Ser Ser Tyr Ile Thr Ser Glu Ile Leu Trp 320 325 330	1489
	GGT TAC CGG TTC ACA CCT GTC CTA ACG ATG GAA GAC GGG TTC TAC GAA Gly Tyr Arg Phe Thr Pro Val Leu Thr Met Glu Asp Gly Phe Tyr Glu 335 340 345 350	1537
	GTT GAC TAC AAC AGC TTC CAT GAG ACC TAT GAG ACC AGC ACC CCG TCC Val Asp Tyr Asn Ser Phe His Glu Thr Tyr Glu Thr Ser Thr Pro Ser 355 360 365	1585

	CTT AGT GCC AAA GAG CTA GCG GAG CTG GCT AAC CGG GCA GAG GTG CCT	1633
	Leu Ser Ala Lys Glu Leu Ala Glu Leu Ala Asn Arg Ala Glu Val Pro	
	370 375 380	
5	CTG AGT TGG TCT GTG TCC AGC AAA CTG AAC CAA CAT GCA GAA TTG GAG	1681
	Leu Ser Trp Ser Val Ser Ser Lys Leu Asn Gln His Ala Glu Leu Glu	
	385 390 395	
10	ACA GAA GAG GAA GAG AAG AAC CCG GAA GAA CTG ACG GAG AGG AAT GGG	1729
	Thr Glu Glu Glu Lys Asn Pro Glu Glu Leu Thr Glu Arg Asn Gly	
	400 405 410	
	TGATGCTGGG CTCCTAGTGT GGATCAAGAA GTGTTCTTC TAAGCTCATC CTCTGACAGA	1789
15	CATTACAGAG AACTGATATA TTTTCCTCC TTCACTGCTT GGAAGAACATT ACCCAGAATT	1849
	CACCCACCCC ATCTGGACCT AGTACATTCT GTTTGGGAAG GTCATCATTA ATTTTACTTA	
	AAGTCGGCGC TGGAGAGATG ACGCCGCGGG CTAAGATGGT TTATTGTTCT TGCAGACGGC	1909
20	CTGGGTTCA	1969
		1978

(2) INFORMATION FOR SEQ ID NO:4:

- 25 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 414 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
- 30 (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

35	Met Thr Met Ala Lys Leu Thr Glu Ser Met Thr Asn Val Leu Glu Gly	
	1 5 10 15	
	Asp Ser Met Asp Gln Asp Val Glu Ser Pro Val Ala Ile His Gln Pro	
	20 25 30	
40	Lys Leu Pro Lys Gln Ala Arg Asp Asp Leu Pro Arg His Ile Ser Arg	
	35 40 45	
45	Asp Arg Thr Lys Arg Lys Ile Gln Arg Tyr Val Arg Lys Asp Gly Lys	
	50 55 60	
	Cys Asn Val His His Gly Asn Val Arg Glu Thr Tyr Arg Tyr Leu Thr	
	65 70 75 80	
50	Asp Ile Phe Thr Thr Leu Val Asp Leu Lys Trp Arg Phe Asn Leu Leu	
	85 90 95	
	Ile Phe Val Met Val Tyr Thr Val Thr Trp Leu Phe Phe Gly Met Ile	
	100 105 110	

Trp Trp Leu Ile Ala Tyr Ile Arg Gly Asp Met Asp His Ile Glu Asp
 115 120 125

Pro Ser Trp Thr Pro Cys Val Thr Asn Leu Asn Gly Phe Val Ser Ala
 5 130 135 140

Phe Leu Phe Ser Ile Glu Thr Glu Thr Thr Ile Gly Tyr Gly Tyr Arg
 145 150 155 160

10 Val Ile Thr Asp Lys Cys Pro Glu Gly Ile Ile Leu Leu Leu Ile Gln
 165 170 175

Ser Val Leu Gly Ser Ile Val Asn Ala Phe Met Val Gly Cys Met Phe
 180 185 190

15 Val Lys Ile Ser Gln Pro Lys Lys Arg Ala Glu Thr Leu Val Phe Ser
 195 200 205

Thr His Ala Val Ile Ser Met Arg Asp Gly Lys Leu Cys Leu Met Phe
 20 210 215 220

Arg Val Gly Asp Leu Arg Asn Ser His Ile Val Glu Ala Ser Ile Arg
 225 230 235 240

25 Ala Lys Leu Ile Lys Ser Lys Gln Thr Ser Glu Gly Glu Phe Ile Pro
 245 250 255

Leu Asn Gln Ser Asp Ile Asn Val Gly Tyr Tyr Thr Gly Asp Asp Arg
 260 265 270

30 Leu Phe Leu Val Ser Pro Leu Ile Ile Ser His Glu Ile Asn Gln Gln
 275 280 285

Ser Pro Phe Trp Glu Ile Ser Lys Ala Gln Leu Pro Lys Glu Glu Leu
 35 290 295 300

Glu Ile Val Val Ile Leu Glu Gly Ile Val Glu Ala Thr Gly Met Thr
 305 310 315 320

40 Cys Gln Ala Arg Ser Ser Tyr Ile Thr Ser Glu Ile Leu Trp Gly Tyr
 325 330 335

Arg Phe Thr Pro Val Leu Thr Met Glu Asp Gly Phe Tyr Glu Val Asp
 340 345 350

45 Tyr Asn Ser Phe His Glu Thr Tyr Glu Thr Ser Thr Pro Ser Leu Ser
 355 360 365

Ala Lys Glu Leu Ala Glu Leu Ala Asn Arg Ala Glu Val Pro Leu Ser
 50 370 375 380

Trp Ser Val Ser Ser Lys Leu Asn Gln His Ala Glu Leu Glu Thr Glu
 385 390 395 400

55 Glu Glu Glu Lys Asn Pro Glu Glu Leu Thr Glu Arg Asn Gly
 405 410

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 2301 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: unknown
 - (D) TOPOLOGY: unknown

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- (ix) FEATURE:
- (A) NAME/KEY: CDS
 - (B) LOCATION: 308..1435

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- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

	CTGAGCTGCC	GTTACATTCA	GGAGAACAG	CAGTGTGGC	GGCTCCAAT	CTCAGAGGGA	60
	ACCTAGGGTA	CTGGGGAGA	TGGTGTCAAG	GACATGGACG	CCAACCCCCA	AGGGTTTCTG	120
20	CTGCTGGCTA	CTCTTCTCTC	CAGGCTCTAC	TTCTGTTCAT	ACGGTCCATA	TCTCCTAGGG	180
	GACCCTGAAA	GCCTAGGAAC	CGACTCTGGC	CATCCATCTC	TCCGGGAAGA	TTATAACCCA	240
25	GAGTGCTTCT	CAGGGGGGAA	GAATTGAAAG	CAAACCAGA	CCCCGCAGGA	TCCCCGCTGC	300
	GGCCGCC	ATG GCG CAG GAG AAC	GCC GCT TTC TCT CCC GGG TCG GAG GAG				349
	Met Ala Glu Asn Ala Ala	Phe Ser Pro Gly Ser Glu Glu					
	1	5	10				
30	CCG CCA CGC CGC GGT CGC CAG CGC TAC GTG GAG AAG GAC GGT CGC						397
	Pro Pro Arg Arg Arg Gly Arg Gln Arg Tyr Val Glu Lys Asp Gly Arg						
	15	20	25	30			
35	TGT AAC GTG CAG CAG GGC AAC GTC CGC GAG ACC TAC CGC TAC CTG ACC						445
	Cys Asn Val Gln Gln Gly Asn Val Arg Glu Thr Tyr Arg Tyr Leu Thr						
	35	40	45				
40	GAC CTG TTC ACC ACG CTG GTG GAC CTG CAG TGG CGC CTC AGA CTG CTC						493
	Asp Leu Phe Thr Thr Leu Val Asp Leu Gln Trp Arg Leu Arg Leu Leu						
	50	55	60				
45	TTC TTC GTG CTC GCC TAC GCG CTC ACT TGG CTC TTC TTC GGT GTC ATC						541
	Phe Phe Val Leu Ala Tyr Ala Leu Thr Trp Leu Phe Phe Gly Val Ile						
	65	70	75				
	TGG TGG CTC ATC GCC TAC GGT CGC GGC GAC CTG GAG CAC CTG GAG GAC						589
	Trp Trp Leu Ile Ala Tyr Gly Arg Gly Asp Leu Glu His Leu Glu Asp						
	80	85	90				
50	ACC GCG TGG ACC CCG TGC GTC AAC AAC CTC AAC GGC TTC GTG GCC GCC						637
	Thr Ala Trp Thr Pro Cys Val Asn Asn Leu Asn Gly Phe Val Ala Ala						
	95	100	105	110			

	TTC CTC TTC TCC ATC GAG ACG GAG ACC ACC ATC GGC TAT GGG CAC CGC Phe Leu Phe Ser Ile Glu Thr Glu Thr Thr Ile Gly Tyr Gly His Arg 115 120 125	685
5	GTC ATC ACC GAC CAG TGT CCC GAG GGC ATC GTG CTG CTG CTG CTG CAG Val Ile Thr Asp Gln Cys Pro Glu Gly Ile Val Leu Leu Leu Gln 130 135 140	733
10	GCT ATC CTG GGC TCC ATG GTG AAC GCT TTC ATG GTG GGC TGC ATG TTC Ala Ile Leu Gly Ser Met Val Asn Ala Phe Met Val Gly Cys Met Phe 145 150 155	781
15	GTC AAG ATC TCG CAG CCC AAC AAG CGC GCC GCC ACT CTC GTC TTC TCC Val Lys Ile Ser Gln Pro Asn Lys Arg Ala Ala Thr Leu Val Phe Ser 160 165 170	829
20	TCG CAC GCC GTG GTG TCT CTG CGC GAC GGG CGC CTC TGT CTC ATG TTT Ser His Ala Val Val Ser Leu Arg Asp Gly Arg Leu Cys Leu Met Phe 175 180 185 190	877
25	CGC GTG GGC GAC CTG CGA TCC TCA CAC ATC GTC GAG GCC TCC ATC CGA Arg Val Gly Asp Leu Arg Ser Ser His Ile Val Glu Ala Ser Ile Arg 195 200 205	925
30	GCC AAG CTC ATC CGC TCC CGT CAG ACG CTC GAG GGC GAG TTC ATC CCT Ala Lys Leu Ile Arg Ser Arg Gln Thr Leu Glu Gly Glu Phe Ile Pro 210 215 220	973
35	TTG CAC CAG ACC GAC CTC AGC GTG GGC TTT GAC ACG GGG GAC GAC CGC Leu His Gln Thr Asp Leu Ser Val Gly Phe Asp Thr Gly Asp Asp Arg 225 230 235	1021
40	CTC TTT CTC GTC TCA CCT CTC GTC ATC AGC CAC GAA ATC GAT GCC GCC Leu Phe Leu Val Ser Pro Leu Val Ile Ser His Glu Ile Asp Ala Ala 240 245 250	1069
45	AGC CCC TTC TGG GAG GCA TCG CGC CGC GCC CTC GAG AGG GAC GAC TTC Ser Pro Phe Trp Glu Ala Ser Arg Arg Ala Leu Glu Arg Asp Asp Phe 255 260 265 270	1117
50	GAG ATC GTA GTC ATT CTC GAG GGC ATG GTG GAG GGC ACG GGA ATG ACG Glu Ile Val Val Ile Leu Glu Gly Met Val Glu Ala Thr Gly Met Thr 275 280 285	1165
55	TGC CAA GCT CGA AGC TCG TAC CTG GTG GAT GAA GTG TTG TGG GGA CAC Cys Gln Ala Arg Ser Ser Tyr Leu Val Asp Glu Val Leu Trp Gly His 290 295 300	1213
	CGG TTC ACA TCC GTG CTC ACC CTG GAG GAT GGT TTC TAT GAG GTG GAC Arg Phe Thr Ser Val Leu Thr Leu Glu Asp Gly Phe Tyr Glu Val Asp 305 310 315	1261
	TAC GCC AGC TTC CAC GAA ACC TTT GAG GTG CCC ACA CCC TCG TGC AGT Tyr Ala Ser Phe His Glu Thr Phe Glu Val Pro Thr Pro Ser Cys Ser 320 325 330	1309

GCT CGG GAA CTG GCA GAA GCC GCG GCC CGC CTT GAT GCC CAT CTC TAC Ala Arg Glu Leu Ala Glu Ala Ala Ala Arg Leu Asp Ala His Leu Tyr 335 340 345 350	1357
5 TGG TCC ATC CCC AGC AGG CTG GAT GAG AAG GTG GAG GAA GAA GGG GCT Trp Ser Ile Pro Ser Arg Leu Asp Glu Lys Val Glu Glu Gly Ala 355 360 365	1405
10 GGG GAG GGG GGC AGG TGC GGG AGA TGG AGC TGACAAGGAG CACAATGGCT Gly Glu Gly Gly Arg Cys Gly Arg Trp Ser 370 375	1455
GCCACCCCCA GAGAGTGAGT CCAAGGTGTG ACTGGTTTCC TCCCACCCCC TGTGGCAGAC	1515
15 CAGGGGGCCG GACTCAGGTA CACAGAACGCT GCGAGTGGAG GTGGAAGAAG AGGAGGCAGG	1575
CAGTGTCCCCG AGGAACAGCT AAAGTTGGGA GAGGCCGCT GAGTCCAGGA TCGAGTAGGG	1635
20 AAGGCTGAGG TCCTGGTTTG AAGAGAGAGG GTTGCAAGGC GGGGTGAGAG AACATGTCAG	1695
TCTGTCTGTG TTTGACCTTC ACATCGGTT ACATGGAT GGATGGACAG AAGGATGGC	1755
TCATGGGGGT TGATCGGGAA GGTGGAGCAG ATAGAGACAG CCAATGGATA ATCGCTCAGG	1815
25 TGGTAAGTGG CTTGGCAGTC GATGATCGTC ACCTGCAGCA CACCTTGAG AGAAATCCAT	1875
GGGCATCCTT TTCTTCAGA TATAGGTAGC CTCAAACCAG GGAGCGTGGC TTAGGGAGCA	1935
GGCTGTCAGG TGGACTACCA CCCCCACTCA CCTCCCTCA ACTGGCCTCC CTGATGTGTG	1995
30 ACACGCCTGC CTAACTAGAG AAGAGAGCAC TGGGTAGAGG TGGACACAGG TGTGGCTGCC	2055
CTCCCCAGTA TCACTGTCCC ATGGCGAGAG GTCAGAAAGG CAAACAAACA ATGGGGTAG	2115
35 ATGCTGAGCA GGGAGGGGCC CTGAAGCAGG ACCTGGGAC AGCCAAGGAC AACTATTTG	2175
TGAGAGAGGA ATGAAACCTT GCAGGTCTG CCACAGAACG AAGAAGCAGA GGAAAGGCCA	2235
40 TGGAGAGACT TAATAAAGGG TTTTACAAGG GAAAAAAA AAAAAAAA AAAAAAAA	2295
AAAAAA	2301

(2) INFORMATION FOR SEQ ID NO:6:

45

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 376 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

50

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

55 Met Ala Gln Glu Asn Ala Ala Phe Ser Pro Gly Ser Glu Glu Pro Pro	
1 5 10 15	

Arg Arg Arg Gly Arg Gln Arg Tyr Val Glu Lys Asp Gly Arg Cys Asn
 20 25 30

Val Gln Gln Gly Asn Val Arg Glu Thr Tyr Arg Tyr Leu Thr Asp Leu
 5 35 40 45

Phe Thr Thr Leu Val Asp Leu Gln Trp Arg Leu Arg Leu Leu Phe Phe
 '50 55 60

10 Val Leu Ala Tyr Ala Leu Thr Trp Leu Phe Phe Gly Val Ile Trp Trp
 65 70 75 80

Leu Ile Ala Tyr Gly Arg Gly Asp Leu Glu His Leu Glu Asp Thr Ala
 85 90 95

15 Trp Thr Pro Cys Val Asn Asn Leu Asn Gly Phe Val Ala Ala Phe Leu
 100 105 110

Phe Ser Ile Glu Thr Glu Thr Thr Ile Gly Tyr Gly His Arg Val Ile
 20 115 120 125

Thr Asp Gln Cys Pro Glu Gly Ile Val Leu Leu Leu Gln Ala Ile
 130 135 140

25 Leu Gly Ser Met Val Asn Ala Phe Met Val Gly Cys Met Phe Val Lys
 145 150 155 160

Ile Ser Gln Pro Asn Lys Arg Ala Ala Thr Leu Val Phe Ser Ser His
 165 170 175

30 Ala Val Val Ser Leu Arg Asp Gly Arg Leu Cys Leu Met Phe Arg Val
 180 185 190

Gly Asp Leu Arg Ser Ser His Ile Val Glu Ala Ser Ile Arg Ala Lys
 35 195 200 205

Leu Ile Arg Ser Arg Gln Thr Leu Glu Gly Glu Phe Ile Pro Leu His
 210 215 220

40 Gln Thr Asp Leu Ser Val Gly Phe Asp Thr Gly Asp Asp Arg Leu Phe
 225 230 235 240

Leu Val Ser Pro Leu Val Ile Ser His Glu Ile Asp Ala Ala Ser Pro
 245 250 255

45 Phe Trp Glu Ala Ser Arg Arg Ala Leu Glu Arg Asp Asp Phe Glu Ile
 260 265 270

Val Val Ile Leu Glu Gly Met Val Glu Ala Thr Gly Met Thr Cys Gln
 50 275 280 285

Ala Arg Ser Ser Tyr Leu Val Asp Glu Val Leu Trp Gly His Arg Phe
 290 295 300

55 Thr Ser Val Leu Thr Leu Glu Asp Gly Phe Tyr Glu Val Asp Tyr Ala
 305 310 315 320

Ser Phe His Glu Thr Phe Glu Val Pro Thr Pro Ser Cys Ser Ala Arg
325 330 335

Glu Leu Ala Glu Ala Ala Arg Leu Asp Ala His Leu Tyr Trp Ser
5 340 345 350

Ile Pro Ser Arg Leu Asp Glu Lys Val Glu Glu Gly Ala Gly Glu
355 360 365

10 Gly Gly Arg Cys Gly Arg Trp Ser
370 375